

 ExPASy Home page

Site Map

Search ExPASy

Contact us

Swiss-Prot

Notice: This page will be replaced with www.uniprot.org. Please send us your feedback!

Search for

UniProtKB/TrEMBL entry Q0PBL7

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#)
[\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	Q0PBL7_CAMJE
Primary accession number	Q0PBL7
Secondary accession numbers	None
Integrated into TrEMBL on	September 19, 2006
Sequence was last modified on	September 19, 2006 (Sequence version 1)
Annotations were last modified on	July 22, 2008 (Entry version 13)
Name and origin of the protein	
Protein name	Major antigenic peptide PEB3 [Precursor]
Synonyms	None
Gene name	Name: peb3 OrderedLocusNames: Cj0289c
From	Campylobacter jejuni [TaxID: 197] [HAMAP proteome]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobact
Protein existence	1: Evidence at protein level;
References	

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=NCTC 11168 / Serotype O:2;

DOI=10.1038/35001088; PubMed=10688204 [NCBI, ExPASy, EBI, Israel, Japan]

Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M., Basham D., Chillingworth Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Per C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Be

B.G.;

"The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.";
Nature 403:665-668(2000).

Comments

- **INTERACTION:**

Q0PBH3:motB; NbExp=1; IntAct=EBI-1192366, EBI-1191146;

Copyright

Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>. Distributed under the Creative Commons Attribution-NoDerivs License.

Cross-references

Sequence databases

EMBL AL111168; CAL34442.1; -; [EMBL / GenBank / DDBJ]
Genomic_DNA. [CoCodingSequence]

PIR G81447; G81447.

3D structure databases

PDB 2HXW; X-ray; 1.60 Å; A/B=21-250.[ExPASy / RCSB / EBI]

PDBsum 2HXW; -.

ModBase Q0PBL7.

Protein-protein interaction databases

IntAct Q0PBL7; -.

Ontologies

GO GO:0005515; Molecular function: protein binding (*inferred from physical interaction from IntAct*).
QuickGo view.

Genome annotation databases

GenomeReviews AL111168_GR; Cj0289c.

KEGG cje:Cj0289c; -.

Phylogenomic databases

HOGENOM Q0PBL7; -.

Genome annotation databases

CMR Q0PBL7; Cj0289c.

Other

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Complete proteome; Signal.

Features



Feature table viewer

Key	From	To	Length	Description	FTId
SIGNAL	1	20	20	Potential.	

CHAIN 21 250 230 Potential. PRO_5000074997

Sequence information

Length: 250 AA [This is the length of the unprocessed precursor]

Molecular weight: 27537 Da [This is the MW of the unprocessed precursor]

CRC64: B2A9AF0630A04065 is a checksum on the sequence

10	20	30	40	50	60
MKKIITLFGA	CALAFSMANA	DVNLYGPGGP	HTALKDIANK	YSEKTGVKVN	VNFGPQATWF
70	80	90	100	110	120
130	140	150	160	170	180
ANKKVRIVVP	EGAGKSNTSG	TGVWEDMIGR	TQDIKTIQNF	RNNIVAFVPN	SGSARKLFAQ
190	200	210	220	230	240
250					
EIFKKYKGWRE					

Q
in
F
fo[View entry in original UniProtKB/TrEMBL format](#)[View entry in raw text format \(no links\)](#)[Request for annotation of this UniProtKB/TrEMBL entry](#)BLAST submission on
BLAST ExPASy/SIB
or at NCBI (USA)Sequence analysis tools: ProtParam,
ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to
SWISS-MODELNPSA Sequence
analysis tools

ExPASy Home page

Site Map

Search ExPASy

Contact us

Swiss-Prot

Hosted by CBR Canada Mirror sites: Australia Brazil China Korea Switzerland

Notice: This page will be replaced with www.uniprot.org. Please send us
your feedback!